MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR
PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF
AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA
LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE
GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH

FIG. 1

TCCGCAGGCGGACCGGGGGCAAAGGAGGTGGCATGTCGGTCAGGCACAGCAGGGTCCTGT
GTCCGCGCTGAGCCGCGCTCTCCCTGCTCCAGCAAGGACC
><Met {trans=1-s, dir=f, res=1}>
ATGAGGGCGCTGGAGGGGCCAGGCCTGTCGCTGCTGTGCCTGGTGTTGGCGCTGCCTGCC
CTGCTGCCGGTGCCGGCTGTACGCGGAGTGGCAGAAACACCCACCTACCCCTGGCGGGAC
GCAGAGACAGGGGAGCGGCTGGTGTGCGCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGG
CCGTGCCGCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAG
TTCTGGAACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAG
GAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTC
GCGCACGCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCC
CCGGGCACCCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCC
AGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCC
CTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCC
CTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCT
TTCCAGGACATCTCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAG
GGCTGGGGTCCGACACCAAGGGCGGGCCGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGG
CTCACGGAGCTCCTGGGGGCGCAGGACGGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTG
CGCGTGGCCAGGATGCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC
TGATCCTGGCCCCCTCTTATTTATTCTACATCCTTGGCACCCCACTTGCACTGAAAGAGG
CTTTTTTTTAAATAAGAAGAAATGAGGTTTNTTAAAAAAAAAAAAAAAAAAAAA

FIG. 2

GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNGG
GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCT
GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC
GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCA
GAACACGCAGTGCCTAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGC
TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCT
GCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG
CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCAT

FIG. 3

```
SEQ ID NO:4    128 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
SEQ ID NO:5      1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCNACTACACG
SEQ ID NO:6      1                                                 G
SEQ ID NO:3      1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG

SEQ ID NO:4    178 CA-TTCTGGAACTACCTGGAGCGC
SEQ ID NO:5     51 CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNGG
SEQ ID NO:6      2 CAGTTCTGGAACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGG
SEQ ID NO:3     51 CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNGG

SEQ ID NO:5    101 GGAGCNTGAGGAGGAGGCANGNGCTTGCCACGCCACCCACAACCGCGCCT
SEQ ID NO:6     52 GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCT
SEQ ID NO:7      1                          GAGGGGCCCCCAGGAGTGGTGGCCGGAGGTG
SEQ ID NO:3    101 GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCT

SEQ ID NO:5    151 GCNGCTGCAGCACCGGNTTCTTCGCGCACGCTGNTTTCTGCTTGGAGCAC
SEQ ID NO:6    102 GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC
SEQ ID NO:7     32 TGGCAGGGGTCAGGTTGCTGGTCCCAGCCTTGCACCCTGAGCTAGGACAC
SEQ ID NO:3    151 GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC

SEQ ID NO:5    201 GCATCGTGTCCACCTGGTGNCGGCGTGATTGCNCCGGGCACCCCCAGCCA
SEQ ID NO:6    152 GCATCGTGTCCACCTGGTGCCGGCGTGATTNCCCCGGGCACCCCCAGCCA
SEQ ID NO:7     82 CAGTTCCCCTGACCCTGTTCTTCCCTCCTGGCTGCAGGCACCCCCAGCCA
SEQ ID NO:8      1 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCA
SEQ ID NO:10     1     CTTGTCCACCTGGTGCCGGCGTGATTNCCC-GGGCACCCCCAGCCA
SEQ ID NO:3    201 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCA

SEQ ID NO:5    251 GAACACGCA-TGCAAAGCCGTG
SEQ ID NO:7    132 GAACACGCAGN-CC-AGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGC
SEQ ID NO:8     51 GAACACGCAG-GCCTAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGC
SEQ ID NO:10    47 GAACACGCAGTGCC-AGCCNT-CCCCCCAGGCACCTTCTCAGCCAGCAGC
SEQ ID NO:9      1                    AGCNGTGCNCCNCAGGCACCTTCTCAGCCAGCAGT
SEQ ID NO:3    251 GAACACGCAGTGCCTAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGC

SEQ ID NO:7    182 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
SEQ ID NO:8    101 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
SEQ ID NO:10    97 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCAACGCCCTGGNC-T
SEQ ID NO:9     36 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
SEQ ID NO:3    301 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT

SEQ ID NO:7    232 GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAG
SEQ ID NO:8    151 GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCT
SEQ ID NO:10   147 GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCT
SEQ ID NO:9     86 GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACGCTGTGCACCAGCT
SEQ ID NO:3    351 GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCT

SEQ ID NO:10   197 GCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG
SEQ ID NO:9    136 GCACTGGCTTCCCCCTCAGCACCAGGGTANCAGGAGCTGAGGAGTGTGAG
SEQ ID NO:3    401 GCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG

SEQ ID NO:10   247 CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCAT
SEQ ID NO:9    186 CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCAT
SEQ ID NO:3    451 CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCAT
```

FIG. 4

```
DNA30942    1          M R A L E G P G L S L L C L V L A L P A L L P V P A V R G V A E T P T Y P W R D . A E T G
hTNFR2      1 M A P V A V W A A L A V G L E L W A A A H A L P A Q V A F T P V . A P E P G S T C R L R E Y Y D Q T

                                        CRD 1                                                  CRD 2
DNA30942   45 E R L V C A Q C P P G T F V Q R P C R R D S P T T C G P C P P R H Y T Q F W N Y L E R C R Y C N V L
hTNFR2     50 A Q M C C S K C S P G Q H A K V F C T K T S D T V C D S C E D S T Y T Q L W N W V P E C L S C G S R

                  CRD 2                                                  CRD 3
DNA30942   95 C G E R E E E A R A C H A T H N R A C R C R T G F F . . . . A H A G . . F C L E H A S C P P G A G V
hTNFR2    100 C S S D Q V E T Q A C T R E Q N R I C T C R P G W Y C A L S K Q E G C R L C A P L R K C R P G F G V

            CRD 3                                                                  CRD 4
DNA30942  139 I A P G T P S Q N T Q C Q P C P P G T F S A S S S S E Q C Q P H R N C T A L G L A L N V P G S S S
hTNFR2    150 A R P G T E T S D V V C K P C A P G T F S N T T S S T D I C R P H Q I C N V V A . . . . I P G N A S

                        CRD 4
DNA30942  189 H D T L C T S C T G F P L S T R V P G A E E C E R A V I D F V A F Q D I S I K R L Q R L L Q A L E A
hTNFR2    196 R D A V C T S T S . . P T R S M A P G A V H L P Q P V S T R S Q H T Q P T P E P S T A P S T S F L L

DNA30942  239 P E G W G P T P . . R A G R A A L Q L K L R R R L T E L L G A Q D G A L L V R L L Q A L R V A R M P
hTNFR2     244 P M G P S P P A E G S T G D F A L P V G L I V G V T A L G L L I I G V V N C V I M T Q V K K K P L .

DNA30942  287 G L E R S V R E R F L P V H
hTNFR2    293 C L Q R E A K V P H L P A D K A R G T Q G P E Q Q H L L I T A P S S S S S S L E S S A S A L D R R A

hTNFR2    343 P T R N Q P Q A P G V E A S G A G E A R A S T G S S D S S P G G H G T Q V N V T C I V N V C S S S D

hTNFR2    393 H S S Q C S S Q A S S T M G D T D S S P S E S P K D E Q V P F S K E E C A F R S Q L E T P E T L L G

hTNFR2    443 S T E E K P L P L G V P D A G M K P S
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FIG. 5

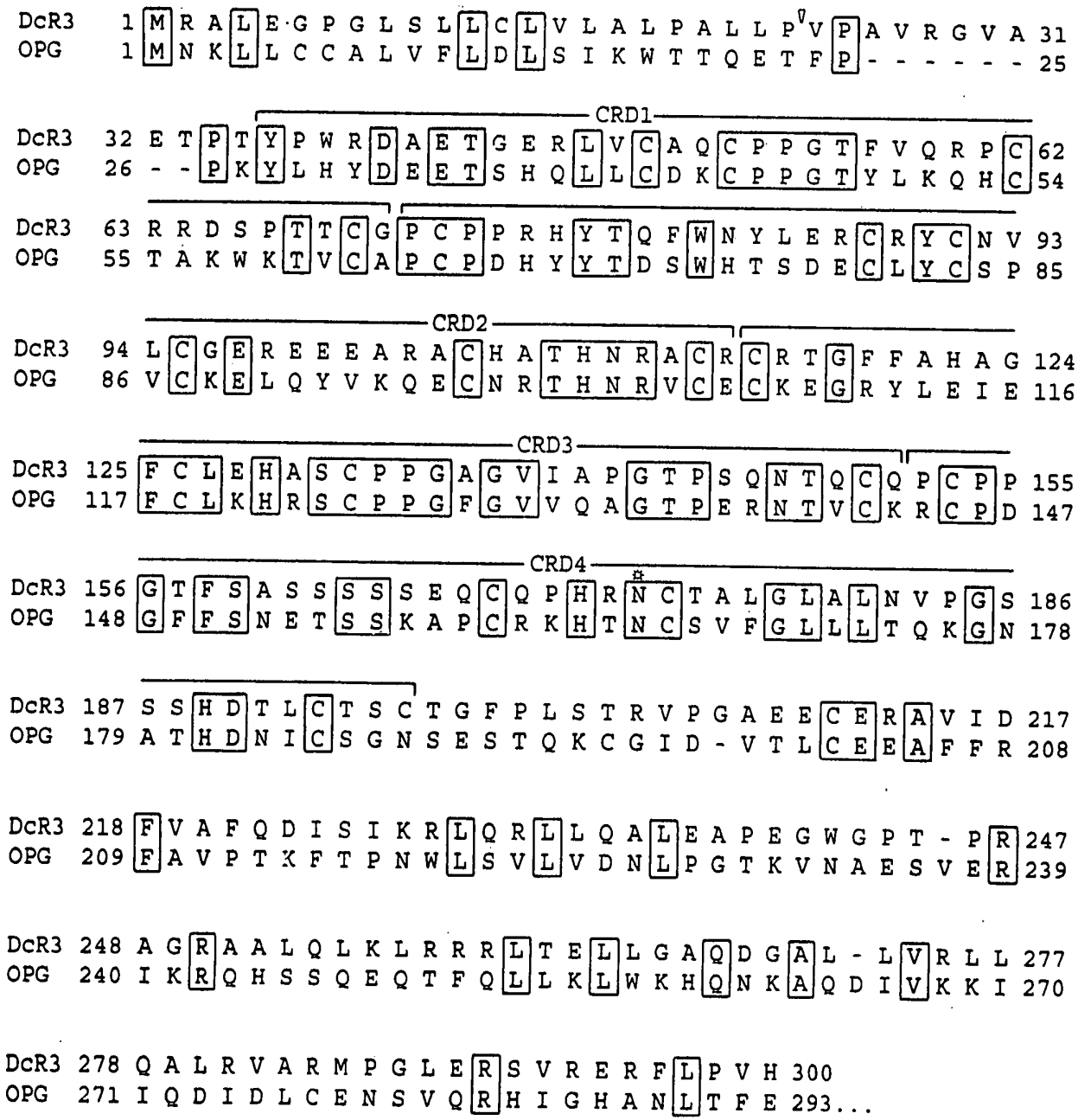


FIG. 6

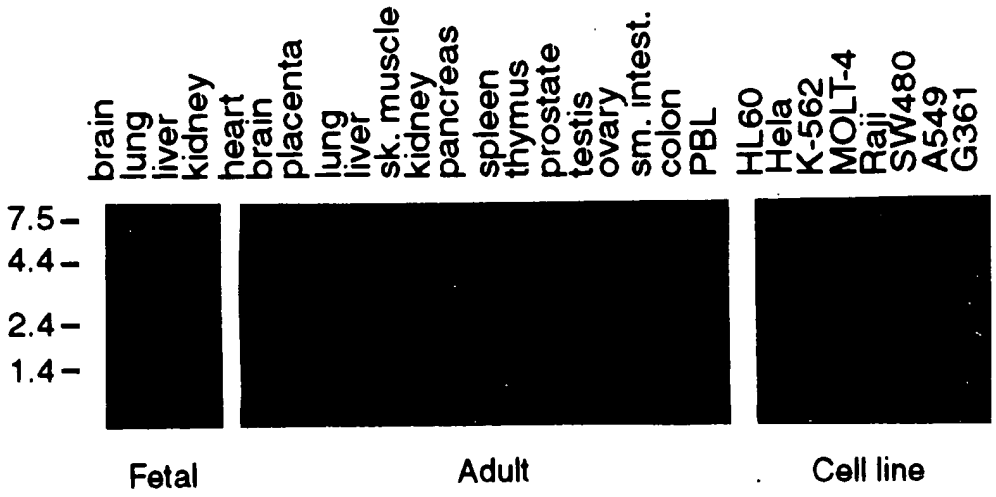


FIG. 7

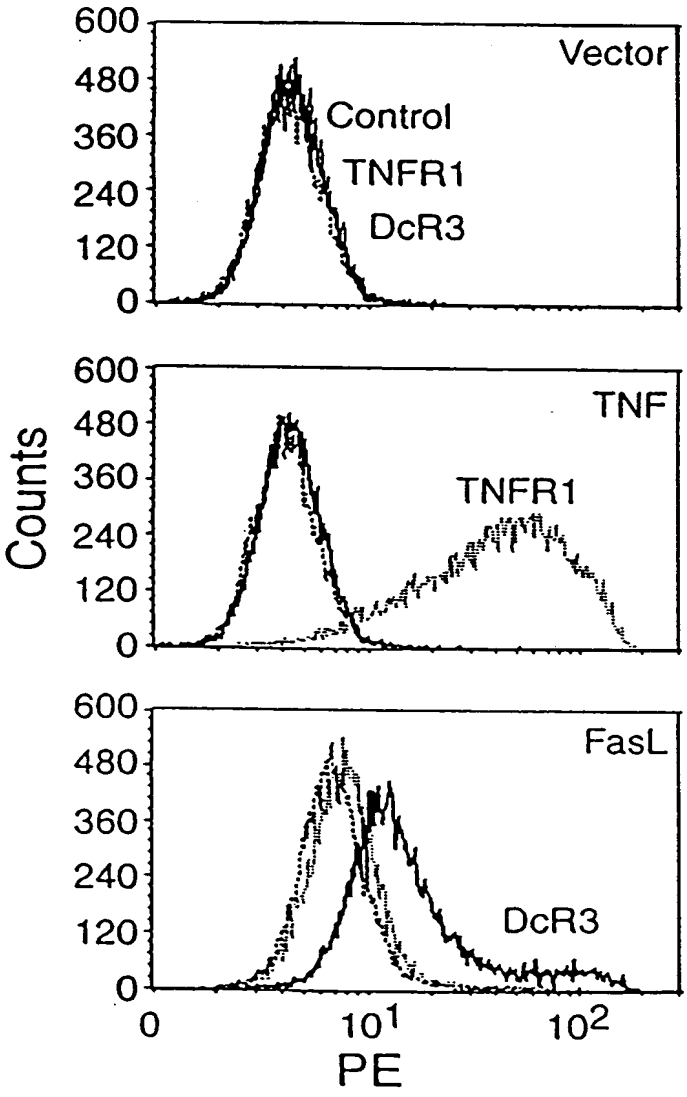


FIG. 8A

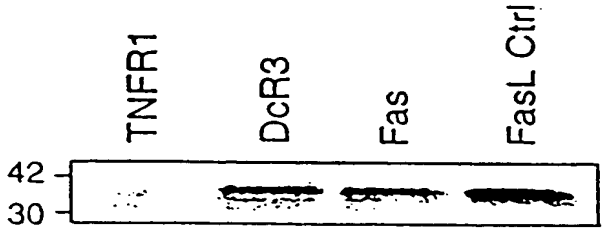


FIG. 8B

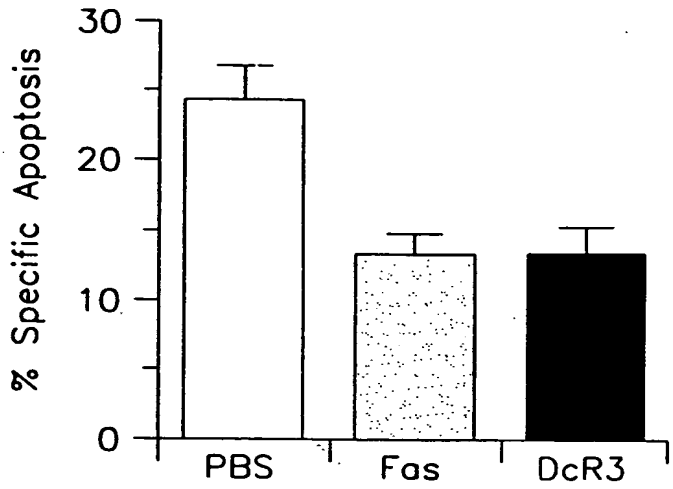


FIG. 9A

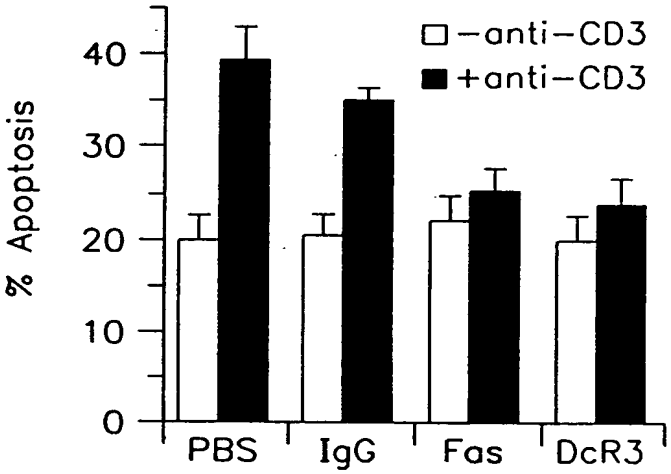


FIG. 9B

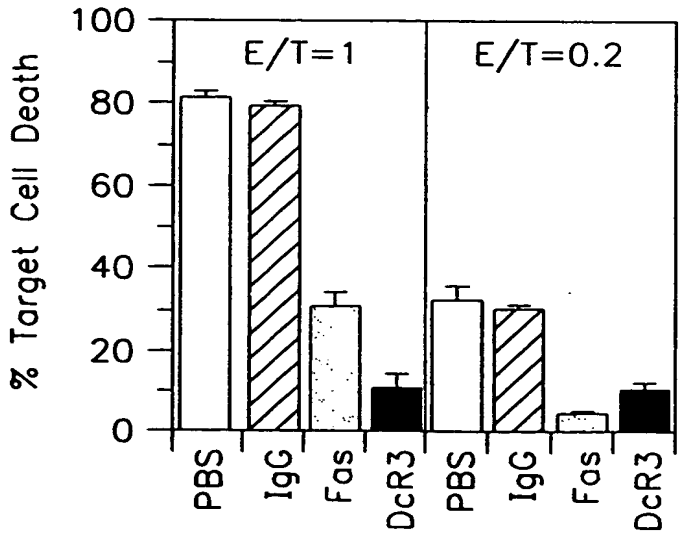


FIG. 9C

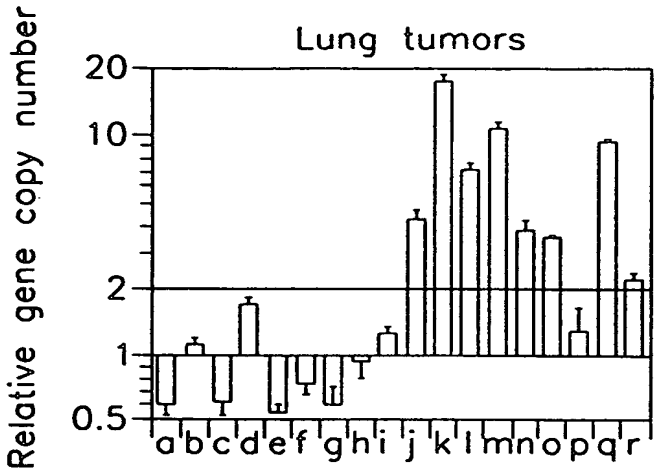


FIG. 10A

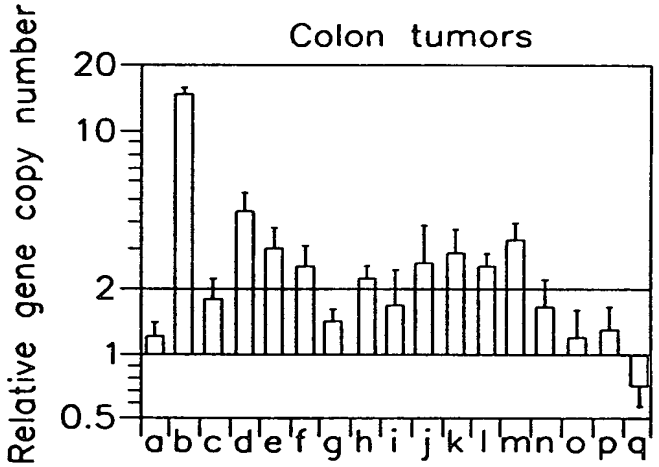


FIG. 10B

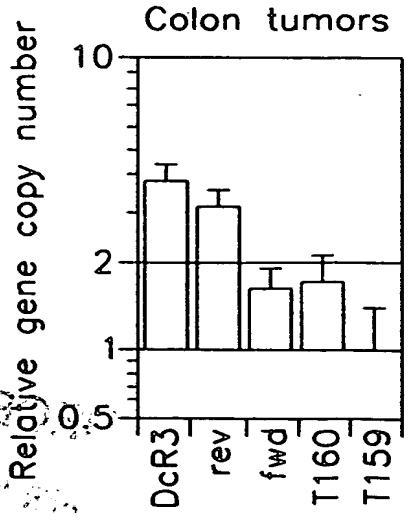


FIG. 10C

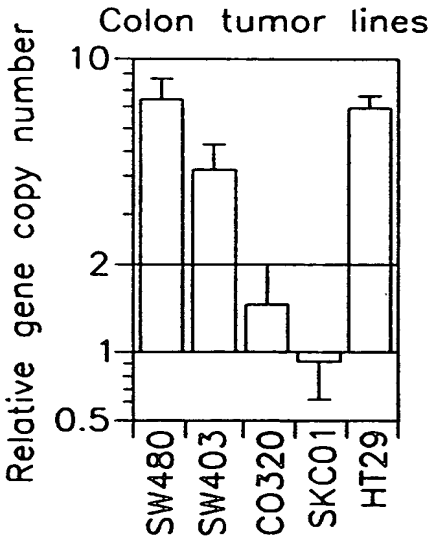


FIG. 10D

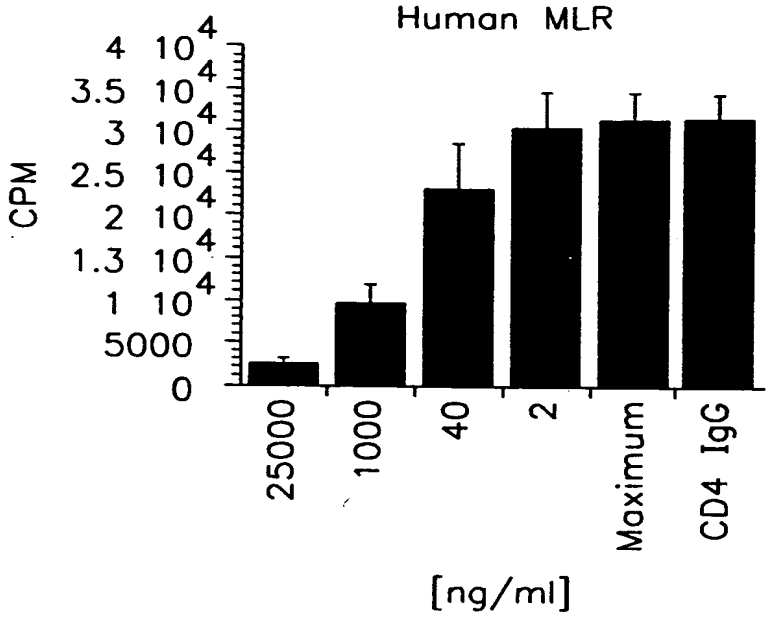


FIG. 1 IA

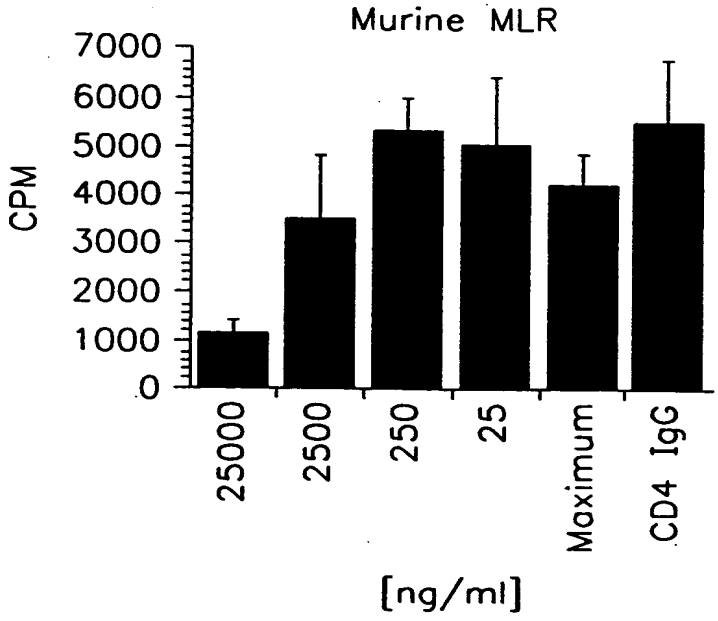


FIG. 1 IB

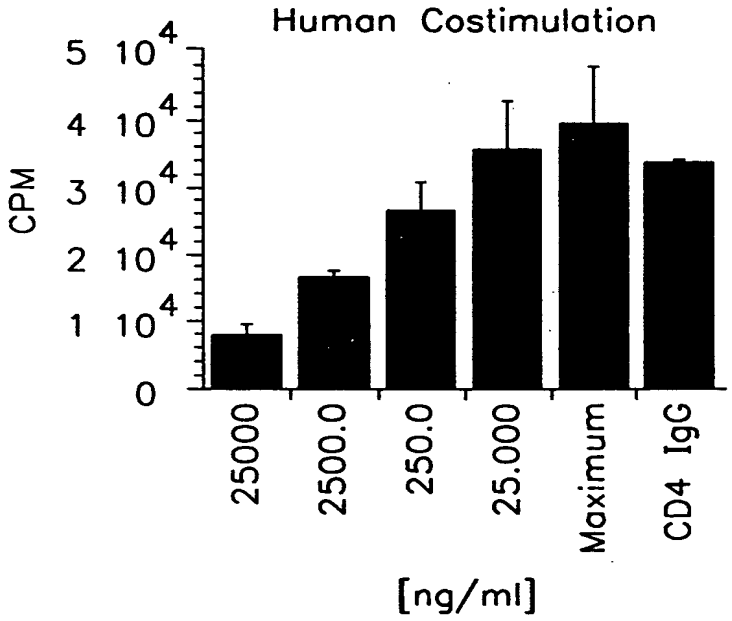


FIG. 1 IC

| mAb | Isotype | Antigen Specitivity (ELISA) DcR3 | DR4 | DR5 | DcR1 | OPG | % Blocking (ELISA) |
|---|---|---|---|---|---|---|---|
| 4B7.1.1 | IgG1 | +++ | - | - | - | - | + |
| 4C4.1.4 | IgG2a | +++ | - | - | - | - | - |
| 5C4.14.7 | IgG2b | +++ | - | - | - | - | ++ |
| 8D3.1.5 | IgG1 | +++ | - | - | - | - | +/- |
| 11C5.2.8 | IgG1 | +++ | - | - | - | - | ++ |

Antigen specificity was determined using 10 microgram/ml mAb.
% blocking activity was determined by ELISA at 100 fold excess of mAb to Fas ligand.

FIG. 12

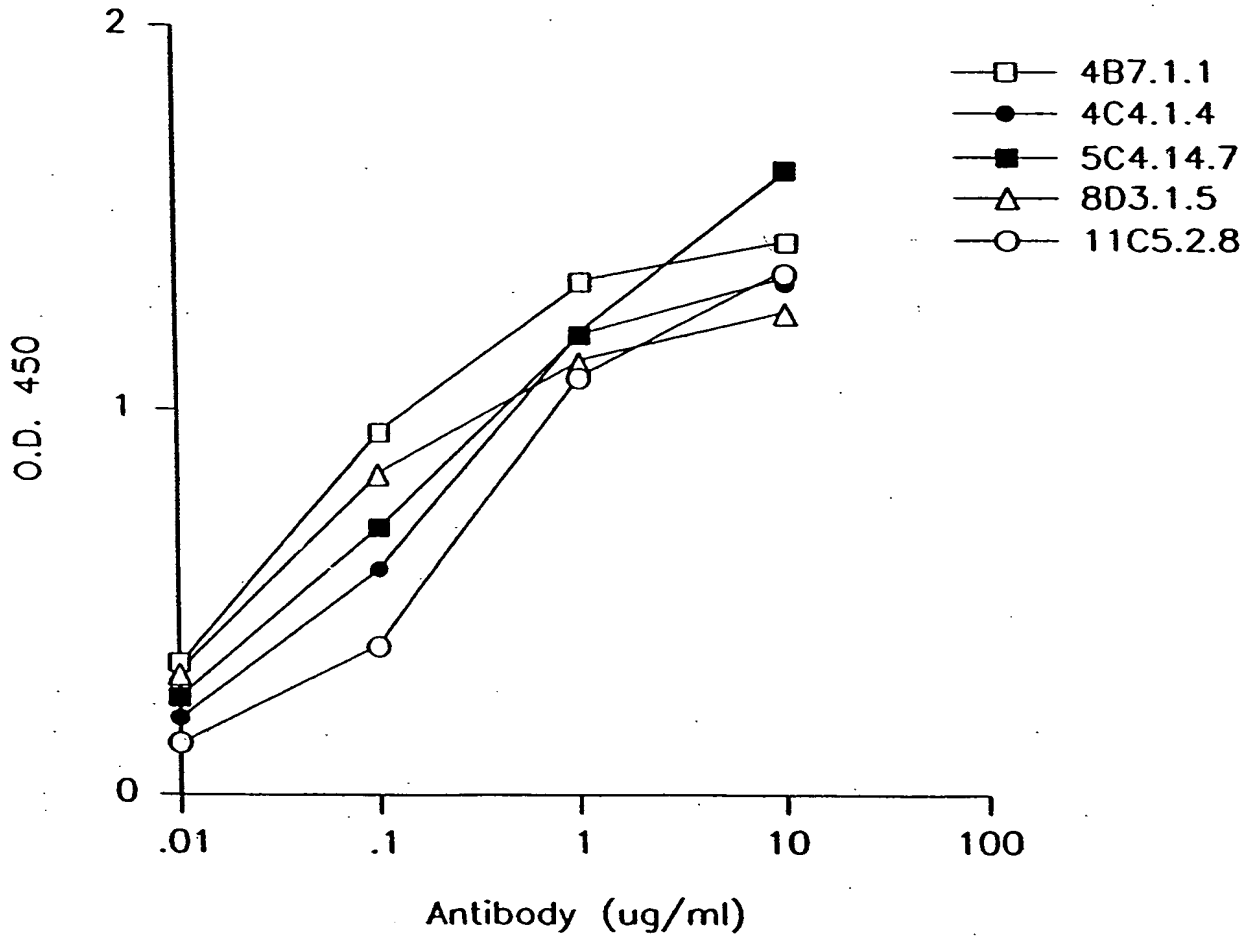


FIG. 13

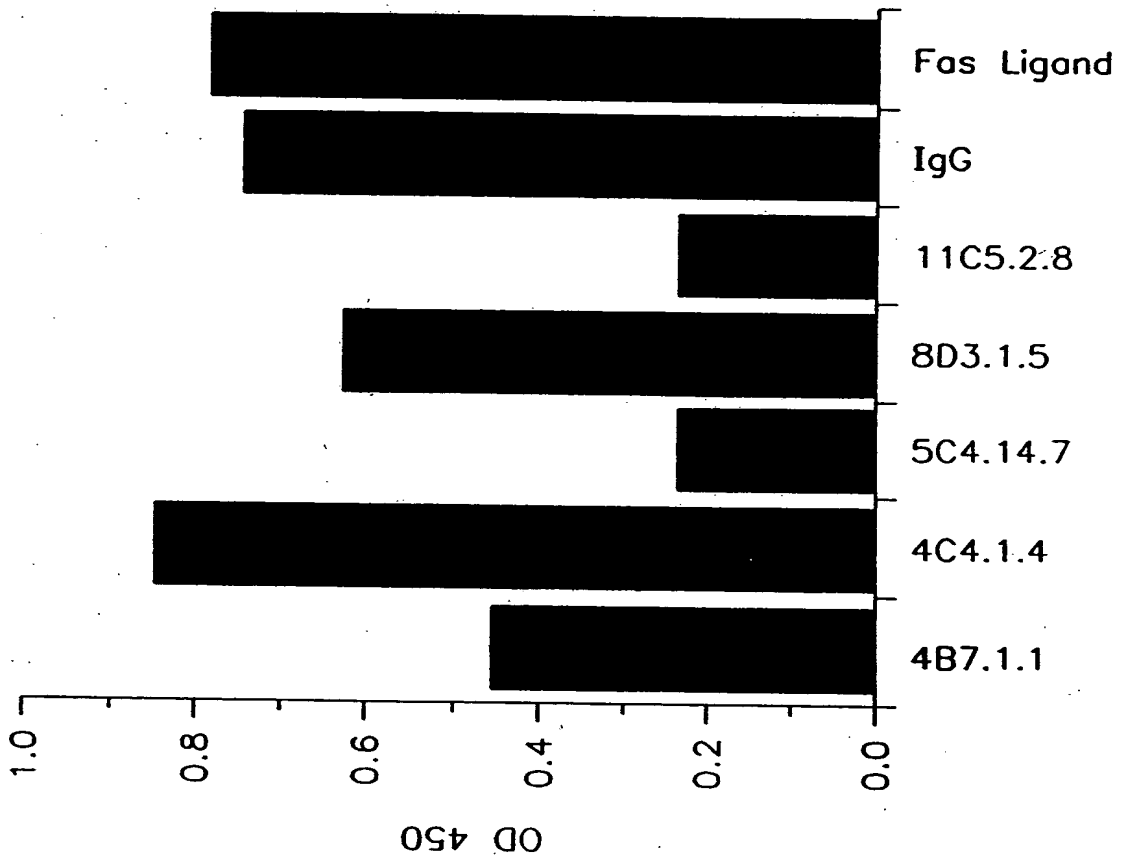


FIG. 14